SEQUENCE LISTING

<110> Fox, Brian A.
Gao, Zeren
Shoemaker, Kimberly E.

<120> NEUROPILIN HOMOLOG ZCUB5

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Arg Ala Ala Gly Arg Gly Leu Leu Ala Leu Leu Leu Ala Val Ser Ala
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ccg ctc cgg ctg cag gcg gag gag ctg ggt gat ggc tgt gga cac cta      207
Pro Leu Arg Leu Gln Ala Glu Glu Leu Gly Asp Gly Cys Gly His Leu
    30                  35                  40
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gtg act tat cag gat agt ggc aca atg aca tct aag aat tat ccc ggg 255
Val Thr Tyr Gln Asp Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly
45 50 55 60

acc tac ccc aat cac act gtt tgc gaa aag aca att aca gta cca aag 303
Thr Tyr Pro Asn His Thr Val Cys Glu Lys Thr Ile Thr Val Pro Lys
65 70 75

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Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asp Ile Glu Ser Gln
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acc tgt gct tct gac tat ctt ctc ttc acc agc tct tca gat caa tat 399
Thr Cys Ala Ser Asp Tyr Leu Leu Phe Thr Ser Ser Ser Asp Gln Tyr
95 100 105

ggt cca tac tgt gga agt atg act gtt ccc aaa gaa ctc ttg ttg aac 447
Gly Pro Tyr Cys Gly Ser Met Thr Val Pro Lys Glu Leu Leu Leu Asn
110 115 120

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Thr Ser Glu Val Thr Val Arg Phe Glu Ser Gly Ser His Ile Ser Gly
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145 150 155

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Thr Cys Leu Glu Arg Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys
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175 180 185

atg gta gat gga tat aga gat acc tct tta ttg tgc aaa gct gcc atc 687
Met Val Asp Gly Tyr Arg Asp Thr Ser Leu Leu Cys Lys Ala Ala Ile
190 195 200

cat gca gga ata att gct gat gaa cta ggt ggc cag atc agt gtg ctt 735
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205 210 215 220

cag cgc aaa ggg atc agt cga tat gaa ggg att ctg gcc aat ggt gtt 783
Gln Arg Lys Gly Ile Ser Arg Tyr Glu Gly Ile Leu Ala Asn Gly Val
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Asn Gly Cys Ser Arg Ser Leu Ser Phe Glu Pro Asp Gly Gln Ile Arg
255 260 265

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Ala Ser Ser Ser Trp Gln Ser Val Asn Glu Ser Gly Asp Gln Val His
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tgg tct cct ggc caa gcc cga ctt cag gac caa ggc cca tca tgg gct 975
Trp Ser Pro Gly Gln Ala Arg Leu Gln Asp Gln Gly Pro Ser Trp Ala
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tcg ggc gac agt agc aac aac cac aaa cca cga gag tgg ctg gag atc 1023
Ser Gly Asp Ser Ser Asn Asn His Lys Pro Arg Glu Trp Leu Glu Ile
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Asp Leu Gly Glu Lys Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser
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Thr Gln Ser Asn Phe Asn Phe Tyr Val Lys Ser Phe Val Met Asn Phe
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Lys Asn Asn Asn Ser Lys Trp Lys Thr Tyr Lys Gly Ile Val Asn Asn
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Asn Asn Phe Ile Pro Pro Ile Val Ala Arg Tyr Val Arg Val Val Pro
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Gln Thr Trp His Gln Arg Ile Ala Leu Lys Val Glu Leu Ile Gly Cys
400 405 410

cag att aca caa ggt aat gat tca ttg gtg tgg cgc aag aca agt caa 1359
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Ala Glu Ala Gln Lys Thr Asp Cys Trp Lys Gln Ile Lys Tyr Pro Phe
495 500 505

gcc aga cat cag tca gct gag ttt acc atc agc tat gat aat gag aag 1647
Ala Arg His Gln Ser Ala Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys
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Gln Gln Pro Leu Met Ile Gly Thr Gly Thr Val Thr Arg Lys Gly Ser
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Thr Phe Arg Pro Met Asp Thr Asp Ala Glu Glu Ala Gly Val Ser Thr
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Asp Ala Gly Gly His Tyr Asp Cys Pro Gln Arg Ala Gly Arg His Glu
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Tyr Ala Leu Pro Leu Ala Pro Pro Glu Pro Glu Tyr Ala Thr Pro Ile
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Val Glu Arg His Val Leu Arg Ala His Thr Phe Ser Ala Gln Ser Gly
605 610 615 620

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Tyr Arg Val Pro Gly Pro Gln Pro Gly His Lys His Ser Leu Ser Ser
625 630 635

ggc ggc ttc tcc ccc gta gcg ggt gtg ggc gcc cag gac gga gac tat 2031
Gly Gly Phe Ser Pro Val Ala Gly Val Gly Ala Gln Asp Gly Asp Tyr
640 645 650

caa agg cca cac agc gca cag cct gcg gac agg ggc tac gac cgg ccc 2079
Gln Arg Pro His Ser Ala Gln Pro Ala Asp Arg Gly Tyr Asp Arg Pro
655 660 665

aaa gct gtc agc gcc ctc gcc acc gaa agc gga cac cct gac tct cag 2127
Lys Ala Val Ser Ala Leu Ala Thr Glu Ser Gly His Pro Asp Ser Gln
670 675 680

aag ccc cca acg cat ccc ggg acg agt gac agc tat tct gcc ccc aga 2175
Lys Pro Pro Thr His Pro Gly Thr Ser Asp Ser Tyr Ser Ala Pro Arg
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gac tgc ctc aca ccc ctc aac cag acg gcc atg act gcc ctt ttg tga 2223
Asp Cys Leu Thr Pro Leu Asn Gln Thr Ala Met Thr Ala Leu Leu *
705 710 715

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Gln Ala Glu Glu Leu Gly Asp Gly Cys Gly His Leu Val Thr Tyr Gln
        35                  40                  45
Asp Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly Thr Tyr Pro Asn
    50                  55                  60
His Thr Val Cys Glu Lys Thr Ile Thr Val Pro Lys Gly Lys Arg Leu
65                  70                  75                  80
Ile Leu Arg Leu Gly Asp Leu Asp Ile Glu Ser Gln Thr Cys Ala Ser
                85                  90                  95
Asp Tyr Leu Leu Phe Thr Ser Ser Ser Asp Gln Tyr Gly Pro Tyr Cys
            100                 105                 110
Gly Ser Met Thr Val Pro Lys Glu Leu Leu Leu Asn Thr Ser Glu Val
        115                 120                 125
Thr Val Arg Phe Glu Ser Gly Ser His Ile Ser Gly Arg Gly Phe Leu
    130                 135                 140
Leu Thr Tyr Ala Ser Ser Asp His Pro Asp Leu Ile Thr Cys Leu Glu
145                 150                 155                 160
Arg Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys Phe Cys Pro Ala
                165                 170                 175
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Gly Cys Arg Asp Val Ala Gly Asp Ile Ser Gly Asn Met Val Asp Gly
180 185 190

Tyr Arg Asp Thr Ser Leu Leu Cys Lys Ala Ala Ile His Ala Gly Ile
195 200 205

Ile Ala Asp Glu Leu Gly Gly Gln Ile Ser Val Leu Gln Arg Lys Gly
210 215 220

Ile Ser Arg Tyr Glu Gly Ile Leu Ala Asn Gly Val Leu Ser Arg Asp
225 230 235 240

Gly Ser Leu Ser Asp Lys Arg Phe Leu Phe Thr Ser Asn Gly Cys Ser
245 250 255

Arg Ser Leu Ser Phe Glu Pro Asp Gly Gln Ile Arg Ala Ser Ser Ser
260 265 270

Trp Gln Ser Val Asn Glu Ser Gly Asp Gln Val His Trp Ser Pro Gly
275 280 285

Gln Ala Arg Leu Gln Asp Gln Gly Pro Ser Trp Ala Ser Gly Asp Ser
290 295 300

Ser Asn Asn His Lys Pro Arg Glu Trp Leu Glu Ile Asp Leu Gly Glu
305 310 315 320

Lys Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser Thr Gln Ser Asn
325 330 335

Phe Asn Phe Tyr Val Lys Ser Phe Val Met Asn Phe Lys Asn Asn Asn
340 345 350

Ser Lys Trp Lys Thr Tyr Lys Gly Ile Val Asn Asn Glu Glu Lys Val
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Phe Gln Gly Asn Ser Asn Phe Arg Asp Pro Val Gln Asn Asn Phe Ile
370 375 380

Pro Pro Ile Val Ala Arg Tyr Val Arg Val Val Pro Gln Thr Trp His
385 390 395 400

Gln Arg Ile Ala Leu Lys Val Glu Leu Ile Gly Cys Gln Ile Thr Gln
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Gly Asn Asp Ser Leu Val Trp Arg Lys Thr Ser Gln Ser Thr Ser Val
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Ser Thr Lys Lys Glu Asp Glu Thr Ile Thr Arg Pro Ile Pro Ser Glu
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Glu Thr Ser Thr Gly Ile Asn Ile Thr Thr Val Ala Ile Pro Leu Val
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Leu Leu Val Val Leu Val Phe Ala Gly Met Gly Ile Phe Ala Ala Phe
465 470 475 480

Arg Lys Lys Lys Lys Lys Gly Ser Pro Tyr Gly Ser Ala Glu Ala Gln
485 490 495

Lys Thr Asp Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln
500 505 510

Ser Ala Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln
515 520 525
Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln Pro Leu
530 535 540
Met Ile Gly Thr Gly Thr Val Thr Arg Lys Gly Ser Thr Phe Arg Pro
545 550 555 560
Met Asp Thr Asp Ala Glu Glu Ala Gly Val Ser Thr Asp Ala Gly Gly
565 570 575
His Tyr Asp Cys Pro Gln Arg Ala Gly Arg His Glu Tyr Ala Leu Pro
580 585 590
Leu Ala Pro Pro Glu Pro Glu Tyr Ala Thr Pro Ile Val Glu Arg His
595 600 605
Val Leu Arg Ala His Thr Phe Ser Ala Gln Ser Gly Tyr Arg Val Pro
610 615 620
Gly Pro Gln Pro Gly His Lys His Ser Leu Ser Ser Gly Gly Phe Ser
625 630 635 640
Pro Val Ala Gly Val Gly Ala Gln Asp Gly Asp Tyr Gln Arg Pro His
645 650 655
Ser Ala Gln Pro Ala Asp Arg Gly Tyr Asp Arg Pro Lys Ala Val Ser
660 665 670
Ala Leu Ala Thr Glu Ser Gly His Pro Asp Ser Gln Lys Pro Pro Thr
675 680 685
His Pro Gly Thr Ser Asp Ser Tyr Ser Ala Pro Arg Asp Cys Leu Thr
690 695 700
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gcgggacc atg ggg acc ggg gct ggt ggg ccg agt gtc ctg gcg ctg ctg 170
Met Gly Thr Gly Ala Gly Gly Pro Ser Val Leu Ala Leu Leu
1 5 10

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ttc gcc gtg tgt gct ccg ctc cgg ttg cag gcg gag gag ctg ggt gat      218
Phe Ala Val Cys Ala Pro Leu Arg Leu Gln Ala Glu Glu Leu Gly Asp
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ggc tgt ggg cac ata gtg acc tct cag gac agt ggc aca atg aca tct      266
Gly Cys Gly His Ile Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser
                35                  40                  45

aag aat tat cca ggg act tac ccc aat tac act gtg tgt gaa aag atc      314
Lys Asn Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile
            50                  55                  60

atc aca gtc cca aag ggg aag aga ctt att ctg agg ttg gga gat ttg      362
Ile Thr Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu
        65                  70                  75

aac att gag tcc aag acc tgc gct tct gac tat ctc ctc ttc agc agt      410
Asn Ile Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser
    80                  85                  90

gca aca gat cag tat ggt cca tat tgt ggg agt tgg gct gtt ccc aaa      458
Ala Thr Asp Gln Tyr Gly Pro Tyr Cys Gly Ser Trp Ala Val Pro Lys
 95                  100                 105                 110

gaa ctc cgg ctg aac tca aac gaa gtg act gtc ctc ttc aag agt gga      506
Glu Leu Arg Leu Asn Ser Asn Glu Val Thr Val Leu Phe Lys Ser Gly
                115                 120                 125

tct cac att tct ggc cgg ggc ttt ctg ctg acc tac gcc agc agt gac      554
Ser His Ile Ser Gly Arg Gly Phe Leu Leu Thr Tyr Ala Ser Ser Asp
            130                 135                 140

cat cca gat tta ata acc tgt ttg gaa cga ggc agc cat tat ttc gag      602
His Pro Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe Glu
        145                 150                 155

gaa aaa tac agc aaa ttc tgc cca gct ggc tgt aga gac ata gca gga      650
Glu Lys Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala Gly
    160                 165                 170

gat att tct ggg aat aca aaa gat ggt tac aga gat acc tct tta ttg      698
Asp Ile Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu
175                 180                 185                 190
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tgc aaa gct gcc atc cac gca ggg atc atc aca gat gaa cta ggt ggc      746
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cac atc aac ttg ctt cag agc aaa ggg ata agt cac tat gaa gga ctc      794
His Ile Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly Leu
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ctg gcc aat ggc gtg ctc tcc cgg cat ggt tct ttg tcg gaa aag cga      842
Leu Ala Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys Arg
        225                 230                 235

ttt ctt ttt aca acc cca gga atg aat att aca act gtg gcg att cca      890
Phe Leu Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile Pro
    240                 245                 250

tca gtg atc ttc atc gcc ctc ctt ctg act gga atg ggg atc ttt gca      938
Ser Val Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe Ala
255                 260                 265                 270

atc tgt aga aag agg aaa aag aaa gga aat cca tat gtg tca gct gac      986
Ile Cys Arg Lys Arg Lys Lys Lys Gly Asn Pro Tyr Val Ser Ala Asp
                275                 280                 285

gct cag aaa aca ggc tgt tgg aag cag att aaa tat ccc ttt gcc agg     1034
Ala Gln Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg
            290                 295                 300

cat cag tcg acg gaa ttt acc atc agc tat gac aat gaa aaa gag atg     1082
His Gln Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met
        305                 310                 315

aca caa aag ttg gat ctc atc act agt gat atg gca gat tat cag cag     1130
Thr Gln Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln
    320                 325                 330

cct ctc atg att ggc aca ggc aca gtc gcg aga aag ggc tct acc ttc     1178
Pro Leu Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr Phe
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cga ccc atg gac aca gac act gag gag gtc aga gtg aac act gag gcc      1226
Arg Pro Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu Ala
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agc ggc cac tat gac tgt cct cac cgc ccg ggc cgc cat gag tac gca      1274
Ser Gly His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr Ala
            370                 375                 380

ctg cct ttg acg cac tca gaa cct gag tat gcc aca cct atc gtg gag      1322
Leu Pro Leu Thr His Ser Glu Pro Glu Tyr Ala Thr Pro Ile Val Glu
        385                 390                 395

cgg cac ctg ctg cga gct cac acc ttc tcc aca cag agc ggc tac cga      1370
Arg His Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr Arg
    400                 405                 410

gtc cct ggg ccc agg ccc act cac aaa cac tcc cat tcc tct gga ggc      1418
Val Pro Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly Gly
415                 420                 425                 430

ttt cct cct gct aca gga gcc acc cag gtt gaa agc tat cag agg cca      1466
Phe Pro Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg Pro
                435                 440                 445

gca agc ccc aag cct gtg ggt ggt ggc tat gac aag cct gct gct agc      1514
Ala Ser Pro Lys Pro Val Gly Gly Gly Tyr Asp Lys Pro Ala Ala Ser
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agc ttc ttg gac agc aga gac cca gcc tct cag tca cag atg act tcc      1562
Ser Phe Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr Ser
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Gly Gly Asp Asp Gly Tyr Ser Ala Pro Arg Asn Gly Leu Ala Pro Leu
    480                 485                 490

aac cag acg gcc atg act gct ctt ttg tga acccaatgtg aaagaaacct        1660
Asn Gln Thr Ala Met Thr Ala Leu Leu  *
495                 500

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gtgactcttc aggatcctag agacgacctc acttactgtt tacagaactg tgcagctggt    1780
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Gly His Ile Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser Lys Asn
        35                  40                  45
Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr
    50                  55                  60
Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile
65                  70                  75                  80
Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr
                85                  90                  95
Asp Gln Tyr Gly Pro Tyr Cys Gly Ser Trp Ala Val Pro Lys Glu Leu
            100                 105                 110
Arg Leu Asn Ser Asn Glu Val Thr Val Leu Phe Lys Ser Gly Ser His
        115                 120                 125
Ile Ser Gly Arg Gly Phe Leu Leu Thr Tyr Ala Ser Ser Asp His Pro
    130                 135                 140
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Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe Glu Glu Lys
145                 150                 155                 160
Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala Gly Asp Ile
                165                 170                 175
Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu Cys Lys
            180                 185                 190
Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly Gly His Ile
        195                 200                 205
Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly Leu Leu Ala
    210                 215                 220
Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys Arg Phe Leu
225                 230                 235                 240
Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile Pro Ser Val
                245                 250                 255
Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe Ala Ile Cys
            260                 265                 270
Arg Lys Arg Lys Lys Lys Gly Asn Pro Tyr Val Ser Ala Asp Ala Gln
        275                 280                 285
Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln
    290                 295                 300
Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln
305                 310                 315                 320
Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln Pro Leu
                325                 330                 335
Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr Phe Arg Pro
            340                 345                 350
Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu Ala Ser Gly
        355                 360                 365
His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr Ala Leu Pro
    370                 375                 380
Leu Thr His Ser Glu Pro Glu Tyr Ala Thr Pro Ile Val Glu Arg His
385                 390                 395                 400
Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr Arg Val Pro
                405                 410                 415
Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly Gly Phe Pro
            420                 425                 430
Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg Pro Ala Ser
        435                 440                 445
Pro Lys Pro Val Gly Gly Gly Tyr Asp Lys Pro Ala Ala Ser Ser Phe
    450                 455                 460
Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr Ser Gly Gly
465                 470                 475                 480
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Asp Asp Gly Tyr Ser Ala Pro Arg Asn Gly Leu Ala Pro Leu Asn Gln
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Thr Ala Met Thr Ala Leu Leu
            500
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<222> (110)...(1486)

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agagccgggc cgggaggccg atcctgcggg tctggagtcc ggcgggacc atg ggg acc    118
                                                      Met Gly Thr
                                                       1

ggg gct ggt ggg ccg agt gtc ctg gcg ctg ctg ttc gcc gtg tgt gct      166
Gly Ala Gly Gly Pro Ser Val Leu Ala Leu Leu Phe Ala Val Cys Ala
     5                  10                  15

ccg ctc cgg ttg cag gcg gag gag ctg ggt gat ggc tgt ggg cac ata      214
Pro Leu Arg Leu Gln Ala Glu Glu Leu Gly Asp Gly Cys Gly His Ile
 20                  25                  30                  35

gtg acc tct cag gac agt ggc aca atg aca tct aag aat tat cca ggg      262
Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly
                 40                  45                  50

act tac ccc aat tac act gtg tgt gaa aag atc atc aca gtc cca aag      310
Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr Val Pro Lys
            55                  60                  65

ggg aag aga ctt att ctg agg ttg gga gat ttg aac att gag tcc aag      358
Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile Glu Ser Lys
        70                  75                  80

acc tgc gct tct gac tat ctc ctc ttc agc agt gca aca gat cag tat      406
Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr Asp Gln Tyr
     85                  90                  95
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gat tta ata acc tgt ttg gaa cga ggc agc cat tat ttc gag gaa aaa      454
Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe Glu Glu Lys
100                 105                 110                 115

tac agc aaa ttc tgc cca gct ggc tgt aga gac ata gca gga gat att      502
Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala Gly Asp Ile
                120                 125                 130

tct ggg aat aca aaa gat ggt tac aga gat acc tct tta ttg tgc aaa      550
Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu Cys Lys
            135                 140                 145

gct gcc atc cac gca ggg atc atc aca gat gaa cta ggt ggc cac atc      598
Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly Gly His Ile
        150                 155                 160

aac ttg ctt cag agc aaa ggg ata agt cac tat gaa gga ctc ctg gcc      646
Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly Leu Leu Ala
    165                 170                 175

aat ggc gtg ctc tcc cgg cat ggt tct ttg tcg gaa aag cga ttt ctt      694
Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys Arg Phe Leu
180                 185                 190                 195

ttt aca acc cca gga atg aat att aca act gtg gcg att cca tca gtg      742
Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile Pro Ser Val
                200                 205                 210

atc ttc atc gcc ctc ctt ctg act gga atg ggg atc ttt gca atc tgt      790
Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe Ala Ile Cys
            215                 220                 225

aga aag agg aaa aag aaa gga aat cca tat gtg tca gct gac gct cag      838
Arg Lys Arg Lys Lys Lys Gly Asn Pro Tyr Val Ser Ala Asp Ala Gln
        230                 235                 240

aaa aca ggc tgt tgg aag cag att aaa tat ccc ttt gcc agg cat cag      886
Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln
    245                 250                 255
```

```
tcg acg gaa ttt acc atc agc tat gac aat gaa aaa gag atg aca caa      934
Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln
260                 265                 270                 275

aag ttg gat ctc atc act agt gat atg gca gat tat cag cag cct ctc      982
Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln Pro Leu
                280                 285                 290

atg att ggc aca ggc aca gtc gcg aga aag ggc tct acc ttc cga ccc     1030
Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr Phe Arg Pro
            295                 300                 305

atg gac aca gac act gag gag gtc aga gtg aac act gag gcc agc ggc     1078
Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu Ala Ser Gly
        310                 315                 320

cac tat gac tgt cct cac cgc ccg ggc cgc cat gag tac gca ctg cct     1126
His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr Ala Leu Pro
    325                 330                 335

ttg acg cac tca gaa cct gag tat gcc aca cct atc gtg gag cgg cac     1174
Leu Thr His Ser Glu Pro Glu Tyr Ala Thr Pro Ile Val Glu Arg His
340                 345                 350                 355

ctg ctg cga gct cac acc ttc tcc aca cag agc ggc tac cga gtc cct     1222
Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr Arg Val Pro
                360                 365                 370

ggg ccc agg ccc act cac aaa cac tcc cat tcc tct gga ggc ttt cct     1270
Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly Gly Phe Pro
            375                 380                 385

cct gct aca gga gcc acc cag gtt gaa agc tat cag agg cca gca agc     1318
Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg Pro Ala Ser
        390                 395                 400

ccc aag cct gtg ggt ggt ggc tat gac aag cct gct gct agc agc ttc     1366
Pro Lys Pro Val Gly Gly Gly Tyr Asp Lys Pro Ala Ala Ser Ser Phe
    405                 410                 415

ttg gac agc aga gac cca gcc tct cag tca cag atg act tcc ggg gga     1414
Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr Ser Gly Gly
420                 425                 430                 435
```

```
gat gat ggt tat tcg gca ccc aga aac ggt ctt gcg ccc ctc aac cag     1462
Asp Asp Gly Tyr Ser Ala Pro Arg Asn Gly Leu Ala Pro Leu Asn Gln
                440                 445                 450

acg gcc atg act gct ctt ttg tga acccaatgtg aaagaaacct gctgtggtac    1516
Thr Ala Met Thr Ala Leu Leu  *
            455

tgagcgcgca ccgctgcgag tcactggaag aaatgtgcaa gcgtgcatgt gtgactcttc   1576
aggatcctag agacgacctc acttactgtt tacagaactg tgcagctggt ttagttccaa   1636
cccttcctgc agagccagtt ggtttctgtt gtgctagaac aaggggactt ttctcatttg   1696
tcttaactgt gatgctgtgc tgtaaaatgt gcaatttgta cagttatatt taacacgaat   1756
taacattacg aagtttgcgg tgtttgtttt ctacacaggg cttaaggaga aaacacggga   1816
tttgtatagc ggtagcctgt gtttctcagt gtatttgatt atctgacgct gtaagcagca   1876
ggtctgttta aaaacctcgt tggttgttgt ggctctttcc tttttgataa agtaaaagca   1936
tttttaccgc tttgtctcct ggaagaaatg aaattacttg aaacatgtaa agcactccag   1996
gataggtgat tgctagcaat ggtggcccat ttatgcaagc aaacatctga ctttagcagc   2056
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aagaaaacat ggaccaaaaa caaacaaaaa atcctttcct tgcaaattgt attataatcc   2716
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<213> Mus musculus

<400> 6

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Gly His Ile Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser Lys Asn
        35                  40                  45
Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr
    50                  55                  60
Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile
65                  70                  75                  80
Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr
                85                  90                  95
Asp Gln Tyr Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe
            100                 105                 110
Glu Glu Lys Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala
        115                 120                 125
Gly Asp Ile Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu
    130                 135                 140
Leu Cys Lys Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly
145                 150                 155                 160
Gly His Ile Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly
                165                 170                 175
Leu Leu Ala Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys
            180                 185                 190
Arg Phe Leu Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile
        195                 200                 205
Pro Ser Val Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe
    210                 215                 220
Ala Ile Cys Arg Lys Arg Lys Lys Lys Gly Asn Pro Tyr Val Ser Ala
225                 230                 235                 240
Asp Ala Gln Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala
                245                 250                 255
Arg His Gln Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu
            260                 265                 270
Met Thr Gln Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln
        275                 280                 285
Gln Pro Leu Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr
    290                 295                 300
Phe Arg Pro Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu
305                 310                 315                 320
Ala Ser Gly His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr
                325                 330                 335
Ala Leu Pro Leu Thr His Ser Glu Pro Glu Tyr Ala Thr Pro Ile Val
            340                 345                 350
Glu Arg His Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr
        355                 360                 365
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```
Arg Val Pro Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly
    370                 375                 380
Gly Phe Pro Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg
385                 390                 395                 400
Pro Ala Ser Pro Lys Pro Val Gly Gly Gly Tyr Asp Lys Pro Ala Ala
                405                 410                 415
Ser Ser Phe Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr
            420                 425                 430
Ser Gly Gly Asp Asp Gly Tyr Ser Ala Pro Arg Asn Gly Leu Ala Pro
        435                 440                 445
Leu Asn Gln Thr Ala Met Thr Ala Leu Leu
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<210> 7
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<212> PRT
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<220>
<223> peptide tag

<400> 7

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<210> 8
<211> 39
<212> PRT
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<220>
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<221> VARIANT
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<223> Xaa is Gly, Arg, Tyr, Ser or Thr

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<223> Xaa is any amino acid

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<223> Xaa is Ser, Thr, Ala, His or Asn

<221> VARIANT
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<223> Xaa is Pro, Leu, Ala or Ile

<221> VARIANT
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<223> Xaa is Asn, Ser, Glu, Asp or His

<221> VARIANT
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<223> Xaa is Tyr, Phe, Trp and Gly

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<400> 8

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30
Xaa Xaa Cys Xaa Xaa Xaa Xaa
        35
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<210> 9
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<213> Artificial Sequence

<220>
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<221> VARIANT
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<223> Xaa is Asp or Glu

<221> VARIANT
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<223> Xaa is Trp, Tyr, Phe, Gln, Ser, Ala, Val or Ile

<221> VARIANT
<222> (6)...(16)
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<221> VARIANT
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<223> Xaa is Gly, Asn, Glu or Met

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<221> VARIANT
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<223> Xaa is Trp, Tyr, Phe, Leu, Ile or Met

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Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Gly
            20                  25
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<210> 10
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<221> VARIANT
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<221> VARIANT
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<221> VARIANT
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<223> Xaa is Lys, Ile, Val or Thr

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<223> Xaa is Gln, Lys or Met

<400> 10

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            20                  25                  30
Xaa Xaa Xaa Gly
        35
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<210> 11
<211> 19
<212> PRT
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<220>
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<221> VARIANT
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<223> Xaa is Leu or Met

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<221> VARIANT
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<221> VARIANT
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<223> Xaa is Leu, Ile, Val or Pro

<221> VARIANT
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<400> 11

Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Xaa Xaa Xaa
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Xaa Gly Cys

<210> 12
<211> 2145
<212> DNA
<213> Artificial Sequence

<220>
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gcnacnccna thgtngarmg ncaygtnytn mgngcncaya cnttywsngc ncarwsnggn 1860
taymgngtnc cnggnccnca rccnggncay aarcaywsny tnwsnwsngg nggnttywsn 1920
ccngtngcng gngtnggngc ncargayggn gaytaycarm gnccncayws ngcncarccn 1980
gcngaymgng gntaygaymg nccnaargcn gtnwsngcny tngcnacnga rwsnggncay 2040
ccngaywsnc araarccncc nacncayccn ggnacnwsng aywsntayws ngcnccnmgn 2100
gaytgyytna cnccnytnaa ycaracngcn atgacngcny tnytn 2145

<210> 13
<211> 1509
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate nucleotide sequence

<221> misc_feature
<222> (1)...(1509)
<223> n = A,T,C or G

<400> 13
atgggnacng gngcnggngg nccnwsngtn ytngcnytny tnttygcngt ntgygcnccn 60
ytnmgnytnc argcngarga rytnggngay ggntgyggnc ayathgtnac nwsncargay 120
wsnggnacna tgacnwsnaa raaytayccn ggnacntayc cnaaytayac ngtntgygar 180
aarathatha cngtnccnaa rggnaarmgn ytnathytnm gnytnggnga yytnaayath 240
garwsnaara cntgygcnws ngaytayytn ytnttywsnw sngcnacnga ycartayggn 300
ccntaytgyg gnwsntgggc ngtnccnaar garytnmgny tnaaywsnaa ygargtnacn 360
gtnytnttya arwsnggnws ncayathwsn ggnmgnggnt tyytnytnac ntaygcnwsn 420
wsngaycayc cngayytnat hacntgyytn garmgnggnw sncaytaytt ygargaraar 480
taywsnaart tytgyccngc nggntgymgn gayathgcng gngayathws nggnaayacn 540
aargayggnt aymgngayac nwsnytnytn tgyaargcng cnathcaygc nggnathath 600
acngaygary tnggnggnca yathaayytn ytncarwsna arggnathws ncaytaygar 660
ggnytnytng cnaayggngt nytnwsnmgn cayggnwsny tnwsngaraa rmgnttyytn 720
ttyacnacnc cnggnatgaa yathacnacn gtngcnathc cnwsngtnat httyathgcn 780
ytnytnytna cnggnatggg nathttygcn athtgymgna armgnaaraa raarggnaay 840
ccntaygtnw sngcngaygc ncaraaracn ggntgytgga arcarathaa rtayccntty 900
gcnmgncayc arwsnacnga rttyacnath wsntaygaya aygaraarga ratgacncar 960
aarytngayy tnathacnws ngayatggcn gaytaycarc arccnytnat gathggnacn 1020
ggnacngtng cnmgnaargg nwsnacntty mgnccnatgg ayacngayac ngargargtn 1080
mgngtnaaya cngargcnws nggncaytay gaytgyccnc aymgnccngg nmgncaygar 1140
taygcnytnc cnytnacnca ywsngarccn gartaygcna cnccnathgt ngarmgncay 1200
ytnytnmgng cncayacntt ywsnacncar wsnggntaym gngtnccngg nccnmgnccn 1260
acncayaarc aywsncayws nwsnggnggn ttyccnccng cnacnggngc nacncargtn 1320
garwsntayc armgnccngc nwsnccnaar ccngtnggng gnggntayga yaarccngcn 1380
gcnwsnwsnt tyytngayws nmgngayccn gcnwsncarw sncaratgac nwsnggnggn 1440
gaygayggnt aywsngcncc nmgnaayggn ytngcnccny tnaaycarac ngcnatgacn 1500
gcnytnytn 1509

<210> 14
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate nucleotide sequence

<221> misc_feature
<222> (1)...(1374)
<223> n = A,T,C or G

<400> 14
atgggnacng gngcnggngg nccnwsngtn ytngcnytny tnttygcngt ntgygcnccn 60
ytnmgnytnc argcngarga rytnggngay ggntgyggnc ayathgtnac nwsncargay 120

wsnggnacna tgacnwsnaa raaytayccn ggnacntayc cnaaytayac ngtntgygar 180
aarathatha cngtnccnaa rggnaarmgn ytnathytnm gnytnggnga yytnaayath 240
garwsnaara cntgygcnws ngaytayytn ytnttywsnw sngcnacnga ycartaygay 300
ytnathacnt gyytngarmg nggnwsncay tayttygarg araartayws naarttytgy 360
ccngcnggnt gymgngayat hgcnggngay athwsnggna ayacnaarga yggntaymgn 420
gayacnwsny tnytntgyaa rgcngcnath caygcnggna thathacnga ygarytnggn 480
ggncayatha ayytnytnca rwsnaarggn athwsncayt aygarggnyt nytngcnaay 540
ggngtnytnw snmgncaygg nwsnytnwsn garaarmgnt tyytnttyac nacnccnggn 600
atgaayatha cnacngtngc nathccnwsn gtnathttya thgcnytnyt nytnacnggn 660
atgggnatht tygcnathtg ymgnaarmgn aaraaraarg gnaayccnta ygtnwsngcn 720
gaygcncara aracnggntg ytggaarcar athaartayc cnttygcnmg ncaycarwsn 780
acngarttya cnathwsnta ygayaaygar aargaratga cncaraaryt ngayytnath 840
acnwsngaya tggcngayta ycarcarccn ytnatgathg gnacnggnac ngtngcnmgn 900
aarggnwsna cnttymgncc natggayacn gayacngarg argtnmgngt naayacngar 960
gcnwsnggnc aytaygaytg yccncaymgn ccnggnmgnc aygartaygc nytnccnytn 1020
acncaywsng arccngarta ygcnacnccn athgtngarm gncayytnyt nmgngcncay 1080
acnttywsna cncarwsngg ntaymgngtn ccnggnccnm gnccnacnca yaarcaywsn 1140
caywsnwsng gnggnttycc nccngcnacn ggngcnacnc argtngarws ntaycarmgn 1200
ccngcnwsnc cnaarccngt nggnggnggn taygayaarc cngcngcnws nwsnttyytn 1260
gaywsnmgng ayccngcnws ncarwsncar atgacnwsng gnggngayga yggntaywsn 1320
gcnccnmgna ayggnytngc nccnytnaay caracngcna tgacngcnyt nytn 1374

<210> 15
<211> 1001
<212> DNA
<213> Homo sapiens

<400> 15
ccgaggacca agttaaacat cctttaggtt atttagctgc acgtcctggc ccctactctg 60
tacactagct tctacatctg gccgtgtacc cacctgttca ctgtgctcca gctacctggc 120
cctttcctcc ttcagcttct ttgcacaact tgtctgtttt ggctcctgct ttaatctcag 180
ctttgatgcc acttaggcct ttcctagctg attcccgccc tcacccctgt tacccgccat 240
ctaattacag ctctctaaat gtgcttcaac agcacctttc atgtcactga ttgcaatttg 300
cattgaatac ttgcctgatt atttttgtct gcaagtgcca catgggttta gccctgctcc 360
tgacaagcac actgctgaac tgagtaactt ttgaatgaat gaatgaatga gtgaataaat 420
cagtgaaggt cctacttggc actgtcatca tcctatcatc aaaatatttc gagtccctcg 480
gtgttgctat ccctggcatg cccatccccg cgggctggca aaaccctgga gggggcagcc 540
tcccaaggca ccgccgcggg ctcagcccat ctaggaatga ctcccgcacc acgcggcgag 600
gggcgggtcc ggcggcgagg tgtcctgctg cctagcaggt tcacgtgtac tggtgcaggt 660
ggggaggaag gcaaggaagg agcgcagcag ggcgcgccag atacgtggag gggagcgcgg 720
gcggcgcctc gctcgcctcc ggcttcgccg tcggtcactg cctgggaacg cgacttcctc 780
ctctaggggc cgacgtgcgg ggcggggcgg ggccgggcgg gagacgcccc cgcagggctg 840
ggctgaaagc cgccccaatg ggattcggtg cggggcagcg actgcgcccc gtcccggcgc 900

cgcgctcgtc cgcagaggag gcggcccggc ccgggcagct gcggctcggg atccgtcgag 960
gggaggccga gcttgccaag ctggcgccca gcggggtcat g 1001

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC28,497

<400> 16
ggcacatagt gacctctcag gacag 25

<210> 17
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC28,498

<400> 17
tcaatgttca aatctcccaa cctca 25

<210> 18
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC28,499

<400> 18
ggtcgctgct cgcataggtc 20

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer ZC28,500

<400> 19
ctgattctga ggttgggaga tttg 24